

=====

Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Jul 26 19:24:33 EDT 2007

=====

Application No: 10519947 Version No: 2.1

Input Set:

Output Set:

Started: 2007-07-26 19:24:23.383
Finished: 2007-07-26 19:24:23.663
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 280 ms
Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 4
Actual SeqID Count: 4

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)

SEQUENCE LISTING

<110> Andersson, Mariette
 Trifonova, Adelina
 Hofvander, Per

<120> Use of AHAS mutant genes as selection marker in potato transformation

<130> 12810-00141-US

<140> US 10/519,947

<141> 2004-12-29

<150> PCT/EP2003/007085

<151> 2003-07-03

<150> EP 02015247.6

<151> 2002-07-09

<160> 4

<170> PatentIn version 3.3

<210> 1

<211> 5717

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (2484)..(4493)

<400> 1

tctagattat gtatttccaa ctttcattaa caatataatc gcatataaat gaaaaatcgt 60

ttccaggata atattttgat gaaatctcat attattgttc gtactcggat tgatgttgaa 120

ggcttgaagc gtttcaaatt atagaccaga ttatttaagt ttttcttttg tttactccat 180

atcaatttga tccattatac tacctaagaa aatttaggta acatagaatt atttattggt 240

atagtaaaaa aaaggaaaac cacaaaaata atctactttt acgtatatac tattttcatg 300

acataagtaa ttaagttgta caactttttt ttaatgaaaa gagagagtaa atttatcatg 360

ttcatgtgta gttacctcgt gaataaccga cggttatata gacgcctaac atgaattggt 420

cagttgaaga cagttcaaaa catgtgtttc actctaaaat cctcaacaaa aaaaaagtgt 480

taaaatttgt aaacctcttt caagcaaaaa aagaaaaagt gttagaatcc caagattctt 540

tcataatccg gaatcttggc tgaaaacgta taaaagagat tgacgtagta acaaggagtc 600

ttggtatgct tccatgcttt ttatcctttt ttgtcatgga accatgattt gggtaccatt 660

tattatgtaa ccgaaatddd cattgtaata atgaatattd aaattdttag caaaaaaaaa 720
caaaaaaaaa caaggagtct tgtcttcgtt ctcaaatttc agagctcttg cacttttcaa 780
gagttttact ttgatgagtg agacatttgt ctttttagtg tttattdtct aaacttaaaa 840
tagtagcatc aacatcactc aattataatt cttaagatgt tgtagaaaaa tattttatag 900
atggaaagta atcgatatta agacaaataa gaaaccaaac cggacttdtg gttcagaccg 960
aatcaaatct gaattggaga aattatggtg gaggcgaaag tcaacggaac taaagtataa 1020
aaccaaatgt caaaaataaa acccaattdt catccttaaa cgaacctgtt gaaaccctaa 1080
tttcgattac caattccgat ctaaaaagaa gtcattggaag ccattgattc cgcaatcgat 1140
cctctcagag atttcgctaa gagcagtggt cgtctcgtcc agcgtgttca caaaccgat 1200
cgcaagggtta acgccttdtc tcaaaaaaat ctcattdccg atttdtgatc tgtagattag 1260
ggtdtdtctga aattdtgata tcatttgtaa ttgaattggg tatcagaatt cacgaaagta 1320
gctgtgcgta cggcgattgg atttgtggtg atgggattcg ttggattctt cgtgaagctc 1380
gttdtcatcc caatcaacaa catcatcgtt ggatcttdtt agtgtagtac ttdcttdtacg 1440
aggtaattga tctcgcatta tatatctaca ttdtggttat gttacttgac atatagtcatt 1500
tgattcaata gtdctgttaa ttdcttdtaa gatcattdtg actagaccac attcttggtt 1560
cattctcaa taattdgtaa tcattatggg ggatatagaa gtagattggg tatagatcag 1620
atagtggaaag acttdaggat gaattdcagc tagtdtdtdt ttdtggtta ttgtctcaaa 1680
agattagtgc ttdgtgtct ccattgcttc tgctatcgac acgcttdctgt ctcttdgtat 1740
cttdattata tctattcgtc ccatgagtdt tgttdgttct gtattcgttc gctctggtgt 1800
catggatgga gtctctgttc catgttdctg taatgcatgt tgggttdgtt catgcaagaa 1860
atgctgagat aaacactcat ttgtgaaagt ttdtaaacct tgaatcgcgc tacaggcaat 1920
gctccgagga gtaggaggag aagaacgaac caaacgacat tatcagccct ttgaggaagc 1980
tcttagtdtdt gtdattgttdt ttgtagccaa attctccatt cttdttccat ttdcacttat 2040
ctcttdgttc ttatagacct tataagtdtdt ttattcatgt atacaaatta tattgtcatc 2100
aagaagtatc ttdaaaatct aaatctcaaa tcaccaggac tatgttdtdtg tccaattcgt 2160
ggaaccaact tgcagcttdt atccattctc ttaaccaata aaaaaagaaa gaaagatcaa 2220
ttdgataaat ttdctagcca caaattctac atttaggttdt tagcatatcg aaggctcaat 2280
cacaaataca atagatagac tagagattcc agcgtcacgt gagtdtdtatc tataaataaa 2340
ggaccaaaaa tcaaatcccg agggcattdt cgtaatccaa cataaaacct ttaacttdca 2400

agttctcattt ttaaacaat catgttcaca agttcttctt tcttctctgt ttctctatct 2460

cttgctcatc tttctcctga acc atg gcg gcg gca aca aca aca aca aca 2513

Met Ala Ala Ala Thr Thr Thr Thr Thr Thr

1

5

10

tct tct tcg atc tcc ttc tcc acc aaa cca tct cct tcc tcc tcc aaa 2561

Ser Ser Ser Ile Ser Phe Ser Thr Lys Pro Ser Pro Ser Ser Ser Lys

15

20

25

tca cca tta cca atc tcc aga ttc tcc ctc cca ttc tcc cta aac ccc 2609

Ser Pro Leu Pro Ile Ser Arg Phe Ser Leu Pro Phe Ser Leu Asn Pro

30

35

40

aac aaa tca tcc tcc tcc tcc cgc cgc cgc ggt atc aaa tcc agc tct 2657

Asn Lys Ser Ser Ser Ser Ser Arg Arg Arg Gly Ile Lys Ser Ser Ser

45

50

55

ccc tcc tcc atc tcc gcc gtg ctc aac aca acc acc aat gtc aca acc 2705

Pro Ser Ser Ile Ser Ala Val Leu Asn Thr Thr Thr Asn Val Thr Thr

60

65

70

act ccc tct cca acc aaa cct acc aaa ccc gaa aca ttc atc tcc cga 2753

Thr Pro Ser Pro Thr Lys Pro Thr Lys Pro Glu Thr Phe Ile Ser Arg

75

80

85

90

ttc gct cca gat caa ccc cgc aaa ggc gct gat atc ctc gtc gaa gct 2801

Phe Ala Pro Asp Gln Pro Arg Lys Gly Ala Asp Ile Leu Val Glu Ala

95

100

105

tta gaa cgt caa ggc gta gaa acc gta ttc gct tac cct gga ggt gca 2849

Leu Glu Arg Gln Gly Val Glu Thr Val Phe Ala Tyr Pro Gly Gly Ala

110

115

120

tca atg gag att cac caa gcc tta acc cgc tct tcc tca atc cgt aac 2897

Ser Met Glu Ile His Gln Ala Leu Thr Arg Ser Ser Ser Ile Arg Asn

125

130

135

gtc ctt cct cgt cac gaa caa gga ggt gta ttc gca gca gaa gga tac 2945

Val Leu Pro Arg His Glu Gln Gly Gly Val Phe Ala Ala Glu Gly Tyr

140

145

150

gct cga tcc tca ggt aaa cca ggt atc tgt ata gcc act tca ggt ccc 2993

Ala Arg Ser Ser Gly Lys Pro Gly Ile Cys Ile Ala Thr Ser Gly Pro

155

160

165

170

gga gct aca aat ctc gtt agc gga tta gcc gat gcg ttg tta gat agt 3041

Gly Ala Thr Asn Leu Val Ser Gly Leu Ala Asp Ala Leu Leu Asp Ser

175

180

185

gtt cct ctt gta gca atc aca gga caa gtc cct cgt cgt atg att ggt 3089

Val Pro Leu Val Ala Ile Thr Gly Gln Val Pro Arg Arg Met Ile Gly

190

195

200

aca gat gcg ttt caa gag act ccg att gtt gag gta acg cgt tcg att 3137

Thr Asp Ala Phe Gln Glu Thr Pro Ile Val Glu Val Thr Arg Ser Ile

205	210	215	
acg aag cat aac tat ctt gtg atg gat gtt gaa gat atc cct agg att			3185
Thr Lys His Asn Tyr Leu Val Met Asp Val Glu Asp Ile Pro Arg Ile			
220	225	230	
att gag gaa gct ttc ttt tta gct act tct ggt aga cct gga cct gtt			3233
Ile Glu Glu Ala Phe Phe Leu Ala Thr Ser Gly Arg Pro Gly Pro Val			
235	240	245	250
ttg gtt gat gtt cct aaa gat att caa caa cag ctt gcg att cct aat			3281
Leu Val Asp Val Pro Lys Asp Ile Gln Gln Gln Leu Ala Ile Pro Asn			
255	260	265	
tgg gaa cag gct atg aga tta cct ggt tat atg tct agg atg cct aaa			3329
Trp Glu Gln Ala Met Arg Leu Pro Gly Tyr Met Ser Arg Met Pro Lys			
270	275	280	
cct ccg gaa gat tct cat ttg gag cag att gtt agg ttg att tct gag			3377
Pro Pro Glu Asp Ser His Leu Glu Gln Ile Val Arg Leu Ile Ser Glu			
285	290	295	
tct aag aag cct gtg ttg tat gtt ggt ggt ggt tgt ttg aat tct agc			3425
Ser Lys Lys Pro Val Leu Tyr Val Gly Gly Gly Cys Leu Asn Ser Ser			
300	305	310	
gat gaa ttg ggt agg ttt gtt gag ctt acg ggg atc cct gtt gcg agt			3473
Asp Glu Leu Gly Arg Phe Val Glu Leu Thr Gly Ile Pro Val Ala Ser			
315	320	325	330
acg ttg atg ggg ctg gga tct tat cct tgt gat gat gag ttg tcg tta			3521
Thr Leu Met Gly Leu Gly Ser Tyr Pro Cys Asp Asp Glu Leu Ser Leu			
335	340	345	
cat atg ctt gga atg cat ggg act gtg tat gca aat tac gct gtg gag			3569
His Met Leu Gly Met His Gly Thr Val Tyr Ala Asn Tyr Ala Val Glu			
350	355	360	
cat agt gat ttg ttg ttg gcg ttt ggg gta agg ttt gat gat cgt gtc			3617
His Ser Asp Leu Leu Leu Ala Phe Gly Val Arg Phe Asp Asp Arg Val			
365	370	375	
acg ggt aag ctt gag gct ttt gct agt agg gct aag att gtt cat att			3665
Thr Gly Lys Leu Glu Ala Phe Ala Ser Arg Ala Lys Ile Val His Ile			
380	385	390	
gat att gac tcg gct gag att ggg aag aat aag act cct cat gtg tct			3713
Asp Ile Asp Ser Ala Glu Ile Gly Lys Asn Lys Thr Pro His Val Ser			
395	400	405	410
gtg tgt ggt gat gtt aag ctg gct ttg caa ggg atg aat aag gtt ctt			3761
Val Cys Gly Asp Val Lys Leu Ala Leu Gln Gly Met Asn Lys Val Leu			
415	420	425	
gag aac cga gcg gag gag ctt aag ctt gat ttt gga gtt tgg agg aat			3809
Glu Asn Arg Ala Glu Glu Leu Lys Leu Asp Phe Gly Val Trp Arg Asn			
430	435	440	

gag ttg aac gta cag aaa cag aag ttt ccg ttg agc ttt aag acg ttt	3857
Glu Leu Asn Val Gln Lys Gln Lys Phe Pro Leu Ser Phe Lys Thr Phe	
445 450 455	
ggg gaa gct att cct cca cag tat gcg att aag gtc ctt gat gag ttg	3905
Gly Glu Ala Ile Pro Pro Gln Tyr Ala Ile Lys Val Leu Asp Glu Leu	
460 465 470	
act gat gga aaa gcc ata ata agt act ggt gtc ggg caa cat caa atg	3953
Thr Asp Gly Lys Ala Ile Ile Ser Thr Gly Val Gly Gln His Gln Met	
475 480 485 490	
tgg gcg gcg cag ttc tac aat tac aag aaa cca agg cag tgg cta tca	4001
Trp Ala Ala Gln Phe Tyr Asn Tyr Lys Lys Pro Arg Gln Trp Leu Ser	
495 500 505	
tca gga ggc ctt gga gct atg gga ttt gga ctt cct gct gcg att gga	4049
Ser Gly Gly Leu Gly Ala Met Gly Phe Gly Leu Pro Ala Ala Ile Gly	
510 515 520	
gcg tct gtt gct aac cct gat gcg ata gtt gtg gat att gac gga gat	4097
Ala Ser Val Ala Asn Pro Asp Ala Ile Val Val Asp Ile Asp Gly Asp	
525 530 535	
gga agc ttt ata atg aat gtg caa gag cta gcc act att cgt gta gag	4145
Gly Ser Phe Ile Met Asn Val Gln Glu Leu Ala Thr Ile Arg Val Glu	
540 545 550	
aat ctt cca gtg aag gta ctt tta tta aac aac cag cat ctt ggc atg	4193
Asn Leu Pro Val Lys Val Leu Leu Leu Asn Asn Gln His Leu Gly Met	
555 560 565 570	
gtt atg caa tgg gaa gat cgg ttc tac aaa gct aac cga gct cac aca	4241
Val Met Gln Trp Glu Asp Arg Phe Tyr Lys Ala Asn Arg Ala His Thr	
575 580 585	
ttt ctc ggg gat ccg gct cag gag gac gag ata ttc ccg aac atg ttg	4289
Phe Leu Gly Asp Pro Ala Gln Glu Asp Glu Ile Phe Pro Asn Met Leu	
590 595 600	
ctg ttt gca gca gct tgc ggg att cca gcg gcg agg gtg aca aag aaa	4337
Leu Phe Ala Ala Ala Cys Gly Ile Pro Ala Ala Arg Val Thr Lys Lys	
605 610 615	
gca gat ctc cga gaa gct att cag aca atg ctg gat aca cca gga cct	4385
Ala Asp Leu Arg Glu Ala Ile Gln Thr Met Leu Asp Thr Pro Gly Pro	
620 625 630	
tac ctg ttg gat gtg att tgt ccg cac caa gaa cat gtg ttg ccg atg	4433
Tyr Leu Leu Asp Val Ile Cys Pro His Gln Glu His Val Leu Pro Met	
635 640 645 650	
atc ccg aat ggt ggc act ttc aac gat gtc ata acg gaa gga gat ggc	4481
Ile Pro Asn Gly Gly Thr Phe Asn Asp Val Ile Thr Glu Gly Asp Gly	
655 660 665	

cgg att aaa tac tgagagatga aaccggtgat tatkagaacc ttttatggtc 4533

Arg Ile Lys Tyr

670

tttgtatgca tatggtaaaa aaacttagtt tgcaatttcc tgtttgttt ggtaatttga 4593

gtttctttta gttgttgatc tgccctgcttt ttggtttacg tcagactact actgctgttg 4653

ttgtttgggt tcctttcttt catTTTTataa ataaataatc cggttcgggt tactccttgt 4713

gactgggtca gtttggttat tgcgaaatgc gaatggtaaa ttgagtaatt gaaattcgtt 4773

attaggggtc taagctgttt taacagtcac tgggttaata tctctcgaat cttgcatgga 4833

aaatgctctt accattgggt ttttaattgaa atgtgctcat atgggccgtg gtttccaaat 4893

taaataaaaac tacgatgtca tcgagaagta aaatcaactg tgtccacatt atcagttttg 4953

tgtatacgat gaaataggggt aattcaaaaat ctagcttgat atgccttttg gttcatttta 5013

accttctgta aacatttttt cagattttga acaagtaa at ccaaaaaaaaa aaaaaaaaaa 5073

tctcaactca aactaaatt attttaaatgt ataaaagatg cttaaaacat ttggcttaaa 5133

agaaagaagc taaaaacata gagaactctt gtaaattgaa gtatgaaaat atactgaatt 5193

gggtattata tgaatttttc tgatttagga ttcacatgat ccaaaaagga aatccagaag 5253

cactaatcag acattggaag taggaatatt tcaaaaagtt tttttttttt aagtaagtga 5313

caaaagcttt taaaaaatag aaaagaaact agtattaaag ttgtaaattt aataaacaaa 5373

agaaattttt tatatttttt catTTTctttt tccagcatga ggttatgatg gcaggatgtg 5433

gatttcattt ttttctttt gatagccttt taattgatct attataattg acgaaaaaat 5493

attagttaat tatagatata ttttaggtag tattagcaat ttacacttcc aaaagactat 5553

gtaagttgta aatatgatgc gttgatctct tcatcattca atgggttagtc aaaaaataa 5613

aagcttaact agtaactaa agtagtcaaa aattgtactt tagtttaaaa tattacatga 5673

ataatccaaa acgacattta tgtgaaacaa aaacaatatc taga 5717

<210> 2

<211> 670

<212> PRT

<213> Arabidopsis thaliana

<400> 2

Met Ala Ala Ala Thr Thr Thr Thr Thr Thr Ser Ser Ser Ile Ser Phe

1

5

10

15

Ser Thr Lys Pro Ser Pro Ser Ser Ser Lys Ser Pro Leu Pro Ile Ser

20

25

30

Arg	Phe	Ser	Leu	Pro	Phe	Ser	Leu	Asn	Pro	Asn	Lys	Ser	Ser	Ser	Ser	35	40	45
Ser	Arg	Arg	Arg	Gly	Ile	Lys	Ser	Ser	Ser	Pro	Ser	Ser	Ile	Ser	Ala	50	55	60
Val	Leu	Asn	Thr	Thr	Thr	Asn	Val	Thr	Thr	Thr	Pro	Ser	Pro	Thr	Lys	65	70	75
Pro	Thr	Lys	Pro	Glu	Thr	Phe	Ile	Ser	Arg	Phe	Ala	Pro	Asp	Gln	Pro	85	90	95
Arg	Lys	Gly	Ala	Asp	Ile	Leu	Val	Glu	Ala	Leu	Glu	Arg	Gln	Gly	Val	100	105	110
Glu	Thr	Val	Phe	Ala	Tyr	Pro	Gly	Gly	Ala	Ser	Met	Glu	Ile	His	Gln	115	120	125
Ala	Leu	Thr	Arg	Ser	Ser	Ser	Ile	Arg	Asn	Val	Leu	Pro	Arg	His	Glu	130	135	140
Gln	Gly	Gly	Val	Phe	Ala	Ala	Glu	Gly	Tyr	Ala	Arg	Ser	Ser	Gly	Lys	145	150	155
Pro	Gly	Ile	Cys	Ile	Ala	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val	165	170	175
Ser	Gly	Leu	Ala	Asp	Ala	Leu	Leu	Asp	Ser	Val	Pro	Leu	Val	Ala	Ile	180	185	190
Thr	Gly	Gln	Val	Pro	Arg	Arg	Met	Ile	Gly	Thr	Asp	Ala	Phe	Gln	Glu	195	200	205
Thr	Pro	Ile	Val	Glu	Val	Thr	Arg	Ser	Ile	Thr	Lys	His	Asn	Tyr	Leu	210	215	220
Val	Met	Asp	Val	Glu	Asp	Ile	Pro	Arg	Ile	Ile	Glu	Glu	Ala	Phe	Phe	225	230	235
Leu	Ala	Thr	Ser	Gly	Arg	Pro	Gly	Pro	Val	Leu	Val	Asp	Val	Pro	Lys	245	250	255
Asp	Ile	Gln	Gln	Gln	Leu	Ala	Ile	Pro	Asn	Trp	Glu	Gln	Ala	Met	Arg	260	265	270
Leu	Pro	Gly	Tyr	Met	Ser	Arg	Met	Pro	Lys	Pro	Pro	Glu	Asp	Ser	His	275	280	285
Leu	Glu	Gln	Ile	Val	Arg	Leu	Ile	Ser	Glu	Ser	Lys	Lys	Pro	Val	Leu	290	295	300
Tyr	Val	Gly	Gly	Gly	Cys	Leu	Asn	Ser	Ser	Asp	Glu	Leu	Gly	Arg	Phe	305	310	315
Val	Glu	Leu	Thr	Gly	Ile	Pro	Val	Ala	Ser	Thr	Leu	Met	Gly	Leu	Gly	325	330	335

Ser Tyr Pro Cys Asp Asp Glu Leu Ser Leu His Met Leu Gly Met His
340 345 350

Gly Thr Val Tyr Ala Asn Tyr Ala Val Glu His Ser Asp Leu Leu Leu
355 360 365

Ala Phe Gly Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu Ala
370 375 380

Phe Ala Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu
385 390 395 400

Ile Gly Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val Lys
405 410 415

Leu Ala Leu Gln Gly Met Asn Lys Val Leu Glu Asn Arg Ala Glu Glu
420 425 430

Leu Lys Leu Asp Phe Gly Val Trp Arg Asn Glu Leu Asn Val Gln